

SAV4029	MVS--TDWKNDL-----RQRGYRLTPORQLVL	25
SCO4180	MVS--TDWKSLL-----RQRGYRLTPORQLVL	25
Franean1DRAFT_3571	MAAKVDDWHTRL-----RARGYRLTPORQLVL	27
Acel_0061	MPKGSSTRPSTRSAQWQRL-----RSKGYRLTPORRLVL	35
Noca_4251	MT--EELAARL-----REQGYRLTPORQLVL	24
Rxy1_1228	MMFEQIL-----RSRGYRLTPORRVIV	23
Rxy1_1140	MTDPPPPGSLSRVVEKFFQLGGDLEAVLGRM-----RGRGYKVTPORLAVL	48
AAur_2630	MGFASIPREVSLSMPQCTSSATTGNEAPATSGVKEQRVTKORLAVS	46
Arth_2638	MAHCAKAEQTKLAPASAGGREQRVTKORLAVS	33
MAV_2036	MTFSGDG-----AGVSVRSTRORAAIS	22
MAP2139	MTFSGDG-----AGVSVRSTRORAAIS	22
Mb2380	MSAAG-----VRSTRORAAIS	16
BCG_2373	MSAAG-----VRSTRORAAIS	16
MT2428	MSAAG-----VRSTRORAAIS	16
Rv2359	MSAAG-----VRSTRORAAIS	16
MUL_3612	MTGTS-----VRSTRORAAIS	16
ML0824	MMTGAS-----VRSTRORAAIS	17
MSMEG_4487	MTGA-----VRSTRORAAIA	15
Mvan_3820	MTGA-----VRSTRORAAIS	15
Mjls_3458	MSPAP-----VRSTRORAAIA	16
Mkms_3510	MSPAP-----VRSTRORAAIA	16
Mmcs_3447	MSPAP-----VRSTRORAAIA	16
nfa14570	MQDKMSAP-----QKP--VGIKSTRORSAIA	24
RHA1_ro01222	MTQMTGQ-----RKPVVVGVRAIKORSAIS	25
SAV5631	MTTAGSP-----VRGRSTRORAAVA	20
SCO2508	MTTAGPP-----VKGRSTRORAAVS	20
Noca_1934	MTSTEHAE-----TF--RLRPTTRORRAVL	22
FRAAL0074	-----MRATROGDVAIC	11
Francia3_0061	MERRPAPSRGT-----AVRATROGDVAIS	23
Franean1DRAFT_4289	MDVVAIVEGERVSSPRGMSAASDRAAGGAGAGSGDRPNGAVSRPGRGRGT-----SVRATROGDVAIS	62
Tfu_0856	-----MSSRR--EAVR	9
Acel_2085	MSGSSSEGR-----QSRSTRORAKALA	20
BAD_0517	MSEHI-----VRQTRQKDAIR	16
BL1128	MTLPMVEHI-----ERQTKQKDAIR	20
Lxxx25010	MV-----KRNFWOREAVR	13
CE2180	MLKKPSRPLRSRIRGNHCFPDSQEGGMGLNRHGEKS-----TPKLGVRSTRORRAVAV	53
NCg12200	MGINRISQGS-----APKLGVRSTRORRAVAV	26
DIP1710	MNRTIDRS-----VFKLGVRSTRORRAVAV	24
jk0612	MSNFAITNK-----LEKIGQRNTRORRAVA	24
PPA0948	MENRR-----RTTKORLAIR	15
FRAAL5117	-----MAVL	4
Francia3_3112	MNDQI-----DLRLTPORMAVL	17
Franean1DRAFT_4643	MPERT-----ELRLTPORTRVL	17
FRAAL2798	MEDRRFVGAAAATAAAGHDALPGRDDLAAAGIAELR-----ALGERVTPARRAVL	51
Francia3_2661	MKDTWIVKDSQTRD-----GRRGDPASAAGIAAALR-----ARGERVTPARRAVL	44
Rxy1_1144	-----MSFRRRTROREAIL	14
SAV3053	MSDLLERLR-----GRGWRMTAORRVVA	23
SCO5206	MSDLLERLR-----GRGWRMTAORRVVA	23
Acel_2095	MRSFVDRLR-----AAGMRVTPARLAVL	23
Noca_0839	MAPAEDLR-----AAGLRVTRPRVAVL	23
Mkms_4974	-----	
Mmcs_4885	-----	
Mjls_5253	MTFARETTPEARLR-----ASGLRVTAAPRLAVL	28
MSMEG_6253	MTVVDHDPKALL-----ASGLRVTAAPRVAVL	28
FRAAL3168	MATDRATTLR-----GAGLRVTGPRLAVL	24
nfa3250	MHTETAEPDRDLR-----AAGLRVTAPRLAVL	27
RHA1_ro04308	MRHDT-DPKAQLR-----EVGLRVTAAPRVAVL	26
Tfu_0145	MDDAASLR-----AAGLRVTAARLAIL	22
Mjls_2712	MAVVSSSSEYVDQLR-----GADLRVTRPRVAVL	29
Mmcs_2681	MITPLGLKSRICLARRPIGVSAQNARDELLTYSKKGDMMAVVSSSSEYVDQLR-----GADLRVTRPRVAVL	67
Mkms_2726	MAVVSSSSEYVDQLR-----GADLRVTRPRVAVL	29
MSMEG_3460	MPSRAEFEAQLR-----MTDLRVTRPRVAVL	26
MAV_2752	-----MADLRVTRPRVAVL	14
MAP1669c	MSSTADYADRLR-----MADLRVTRPRVAVL	26
MUL_2189	-----MADLRVTRPRVAVL	14
Mb1944c	MSSVSSIPDYAEQLR-----TADLRVTRPRVAVL	29
MT1960	MSSVSSIPDYAEQLR-----TADLRVTRPRVAVL	29
Rv1909c	MSSVSSIPDYAEQLR-----TADLRVTRPRVAVL	29
BCG_1948c	MSSVSSIPDYAEQLR-----TADLRVTRPRVAVL	29
RHA1_ro05274	MPDYAALLR-----GAELRVTRPRVAVL	23
Mvan_2983	MTSDYAEALLR-----GADLRVTRPRVAVL	24
Franean1DRAFT_1681	MVAWLLSGFLDWFQKMGDEVVVATAEDFRMLR-----GAALRVTRPRVAVL	47
Noca_0874	MATTIDTRDFPELLR-----GAALRVTRPRVAVL	24
MSMEG_6383	---MTHTTDFEQLLR-----SAGMRVTRPRVAVL	30
Mvan_3209	MEPMTEEPDYSAVLR-----SAALRVTRPRVAVL	29
nfa29490	MASKVPDFEQLLR-----GASLRVTAORLAVL	26
SCO0561	MTASRNSRKPAIADELRL-----RAGLRVTAARVALL	31
FurS	MTASF--TPTAEELR-----GAGLRVTAARVALL	28
AAur_3058	MMDHTTEQAEWAAALH-----AHGRRVTKORLAVL	30
Arth_3077	MVVEHAGQDAWAAALR-----AHGRRVTKORLAVL	30
Lxxx02790	MDTAQLEDTLR-----SAGLRVTRGRVAVL	25
Rxy1_1224	MAGFCMTERLEEDIREKFR-----RSQVTLTSORRAVL	33
Mjls_1895	MAAAVEDGVG-----VLVKKRVQLRRRCDA	26
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80	



SAV4029 EAVDKLE-HAIPDDILVEVRKKTASGVNISTVVRTLELELEELGLVSHAHLGHGAPT VHLADRH---HHIHLVCRDCTNVIE 101
SCO4180 EAVDTLE-HAIPDDILGVRKKTASGINISTVVRTLELELEELGLVSHAHLGHGAPT VHLADRH---HHIHLVCRDCTNVIE 101
Franean1DRAFT 3571 EAVARLG-HAIPPEALVHVEVRQTASGVNISTVVRTLELELEELGLVSHAHLGHGAPT VHTVGD---PHVHLVCGACGAILE 103
Acel 0061 EAVAAALR-HAIPPEELINIVREVASGVNMSVTVVRTLDLLEELSLVHTHLGHGAPT VHAEDA---GHVHLVCSGCAVTE 111
Noca 4251 QAVEKLG-HAIPDEVLAEVHAQSSAVNVSTIIVRTLEVLLEELGLVRHAHLSDRAPTVHSVTDR---EHFHLVCRNCHKVVS 100
Rxy1 1228 RELEGER-HLSAEETIYERVKEHEPELGLSTVVRTLDLLEELGIVRKEDFEGEYSRVELATER---MHHHARCRCGCKVIE 99
Rxy1 1140 EALAAER-HQSLLEELRGR---PEVGLATLVRTLDLTTGIGAVRRELELGDG-PRVELAGD---HHHHLICEACGEISE 118
AAur 2630 AALDELDFVSTQELRYRLLNKRGISVSLATAYRILQSLADDGLIDVLRNGDGEAVVRRCAV---TGHHHLLCRNCGKAE 124
Arth 2638 AALDELDFVSTQELRYRLNQGTSVSLATAYRILQSLADDGLVDVLRNGDGEAVVRRCAV---TGHHHLLCRNCGKAE 111
MAV 2036 TLELETVDFFRSAQELHDELRRRGENIGLTVVVRTLQSMASAAGLIDTLRDTGESVYRRCSS---EHHHHLLVCRSCGSTIE 99
MAP2139 TLELETVDFFRSAQELHDELRRRGENIGLTVVVRTLQSMASAAGLIDTLRDTGESVYRRCSS---EHHHHLLVCRSCGSTIE 99
Mb2380 TLELETVDFFRSAQELHDELRRRGENIGLTVVVRTLQSMASGLVDTLRDTGESVYRRCSS---EHHHHLLVCRSCGSTIE 93
BCG 2373 TLELETVDFFRSAQELHDELRRRGENIGLTVVVRTLQSMASGLVDTLRDTGESVYRRCSS---EHHHHLLVCRSCGSTIE 93
MT2428 TLELETVDFFRSAQELHDELRRRGENIGLTVVVRTLQSMASGLVDTLRDTGESVYRRCSS---EHHHHLLVCRSCGSTIE 93
Rv2359 TLELETVDFFRSAQELHDELRRRGENIGLTVVVRTLQSMASGLVDTLRDTGESVYRRCSS---EHHHHLLVCRSCGSTIE 93
MUL 3612 TLELETVDFFRSAQELHDELRRRGENIGLTVVVRTLQSMASAGVVDTLRDTGESVYRRCSS---QHHHHLLVCRSCGSTIE 93
ML0824 TLELETVDFFRSAQELHDELRRRGNISLTVVVRTLQSMASAGVVDTLRDTGESVYRRCSS---RQHHLVCRGCGSTIE 94
MSMEG 4487 DLLNETIEFRSAQELHDELRRRGENIGLTVVVRTLQAMATAGVVDTLRDTGESVYRRCSS---EHHHHLLVCRSCGSTIE 92
Mvan 3820 ALLNEDIEFRSAQELHDELRRRGENIGLTVVVRTLQMAAAGVVDTLRDTGESVYRRCSS---EHHHHLLVCRACGCTVE 96
Mjls 3458 DLLDGLDEFRSAQELHDLAKRRREGIGLTVVVRTLQSMASGLVDVLRDTGESVYRRCSS---ADHHLVCRACGAIVE 93
Mkms 3510 DLLDGLDEFRSAQELHDLAKRRREGIGLTVVVRTLQSMASGLVDVLRDTGESVYRRCSS---ADHHLVCRACGAIVE 93
Mmcs 3447 DLLDGLDEFRSAQELHDLAKRRREGIGLTVVVRTLQSMASGLVDVLRDTGESVYRRCSS---ADHHLVCRACGAIVE 93
nfa14570 ALLGDIDEFRSAQELHDELRRRGENIGLTVVVRTLQSLADAGVVDVLRDTGESVYRRCSS---SGHHHLVCRHCGRTVE 101
RHA1_ro01222 ALLDIEIEFRSAQELHDELRRRGENIGLTVVVRTLQSLADAGVVDVLRDTGESVYRRCSS---SGHHHLVCRHCGRTVE 102
SAV5631 AALDEVDFRSAQELHDMMLKHKGDSVGLTTVVVRTLQNLADAGEVDVLRSDGESVYRRCSS---GEHHHLVCRVCGKAVE 98
SCO2508 AALQEVDFRSAQELHDMMLKHKGDAVGLTTVVVRTLQSLADAGEVDVLRSAEGESVYRRCST---GDHHLVCRACGKAVE 98
Noca 1934 EALDSFDFRSAQELHELLGRREGTVGLATVVRTLQVLAAGEVDVLRLEDGEAIVRRCAT---EAHHHLVCRSCGATVE 99
FRAL0074 AALTEIDAFRSAQELHALLSRGAGVGLTTVVVRHLQVLDVDRGEMVRRDDGETVYRRCAT---EAHHHLVCRCLCGRTVE 89
Franci3 0061 AALAEIDAFRSAQELHALLSRGAGVGLTTVVVRHLQVLDVDRGEMVRRDDGETVYRRCAT---EAHHHLVCRCLCGRTVE 89
Franean1DRAFT 4289 SALAAIDAFRSAQELHALLSRGAGVGLTTVVVRHLQVLDVDRGEMVRRDDGETVYRRCAT---EAHHHLVCRCLCGRTVE 140
Tfu 0856 QALHKSDFRSAQELHALLSRGAGVGLTTVVVRHLQVLDVDRGEMVRRDDGETVYRRCAT---EAHHHLVCRCLCGRTVE 87
Acel 2085 QVMAESDFRSAQELHEALIDRGEVGLTTVVVRTLQSLADAGEVDVLRSDGESVYRRCST---GEHHHLVCRVCGKAVE 98
BAD 0517 DALNCGDFRSAQELHDLAKRRREGIGLTVVVRTLQSMASGLVDVLRDTGESVYRRCSS---ADHHLVCRACGAIVE 93
BL1128 AALADCEEFISADLHRLLEDEGSKIGLATVVRQLNALADAGADTIR-LDGGQLFRLCGD---DGHHHLVCRRCGKAVE 97
Lxx25010 EALSSTIEGFI SAQGLHLRLHEAGSPIGLATVVRALADLAEGDADSLQSPFEGESLYRRCST---GHHHLICRNCGLTVE 90
CE2180 DILEEIDNFSAKATHAELNAREHSVGLTTVVVRTLQSLAEIGAVDVLTVTGGELVRQCHD---EGHHHLVCRQCGRTVE 131
NCg12200 DVLEEIDNFSAKETHHELSTREHNVGLTTVVVRTLQSLADAGEVDVLRSDGESVYRRCST---GEHHHLVCRVCGKAVE 98
DIP1710 QVLDGLDYFAKAVIHQELTKRDLKVLGTVVVRTLQSLAEIGAVDVLHMSNGELVRHCLV---DEHHHLVCRVCGRTVE 104
jk0612 ELLEGLTTFSSAQDIDHQLVAGDQHKVGLTTVVVRTLQMAEAGCIDTLYDSDGETLVRACAT---DDHHHLVCRVCGRTVE 102
PPA0948 ALFDDIEFFLTAQVHQDQLNRGDDQVGLATVVRNLQTMADGEDLDAIRAEDGEMTVYRRCSS---SAHHHLVCRNCGKAVE 92
FRAL5117 EVLRAADDPHAAEVYRVRASPRIGSATVVRTLALLVSGRALELNLGDGAAARYDAN---TRRHDAVCRGCAIRD 81
Franci3 3112 AVLAAARDPHAAEVYRVRASPRIGSATVVRTLALLVSGRALELNLGDGAAARYDAN---TSRHDAVCRGCAIRD 94
Franean1DRAFT 4643 EVLKAARDPHAAEVYRVRASPRIGSATVVRTLALLVSGRALELNLGDGAAARYDAN---TSRHDAVCRGCAIRD 94
FRAL2768 RVLGATSEHLSVDDVLTTRADEIVPGLHRTVVRALETLQELGLVTVHVHPDHGPAVHSLASSLGGSHLVRRCRCGQI 131
Franci3 2991 QVLAGTSEHLSVDDVLTTRADEIVPGLHRTVVRALETLQELGLVTVHVHPDHGPAVHSLASSLGGSHLVRRCRCGQI 124
Rxy1 1144 AALRDAPGPLSAARIREAAREAPGLGRATVVRALRTRLEELVSVVVELPGEPLVSSG---RGEHHHFCRCGGSILD 91
SAV3053 EVLDGDHVLHAADEVHARAVKLPETISRAVNTLQELVSLGEVLEVAIDKRAKRVDPNAHR---PHHHLVCRACGAIRD 100
SCO5206 EVLDGDHVLHAADEVHARAVKLPETISRAVNTLQELVSLGEVLEVAIDKRAKRVDPNAHR---PHHHLVCRACGAIRD 100
Acel 2095 QELVFGV-HRSVDEIATAVRRTLGAVSLQAVNVLDLALAGLVRRIEPLGHPARVESRVS---DNHHHLVCRVCGAIAD 99
Noca 0839 AEVSEHP-HADVDTLATAARALRGKVSQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 99
Mkms 4974 -----MREALGKVSQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 59
Mmcs 4885 -----MREALGKVSQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 59
Mjls 5253 SALAQAP-HSADDVAKQVREALGKVSQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 104
MSMEG 6253 EVLAEQP-HSADDVAMAVRNLGKVSQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 104
FRAL3168 DVLAEHP-HADADAVAEVRRLGTVSKQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 100
nfa3250 KAVSAHP-HADADTAAEVRALGKVSQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 103
RHA1_ro04308 NAVAVRP-HSDVDDIAAVVREELGKVSQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 102
Tfu 0145 HDVRRQN-HLDADRVARVREELGKVSQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 98
Mjls 2712 EAVHARP-HADETIFATVRRSLP DVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 105
Mmcs 2681 EAVHARP-HADETIFATVRRSLP DVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 143
Mkms 2726 EAVHARP-HADETIFATVRRSLP DVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 105
MSMEG 3460 EAVHARP-HADETIYSVVRGSLP TVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 102
MAV 2752 EVVDANP-HADETIFSAVRMALP DVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 90
MAP1669c EVVDANP-HADETIFSAVRMALP DVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 102
MUL 2189 EAVGHEP-HADETIYSAVREILP DVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 90
Mb1944c EAVNAHP-HADETIFGAVRFALP DVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 105
MT1960 EAVNAHP-HADETIFGAVRFALP DVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 105
Rv1909c EAVNAHP-HADETIFGAVRFALP DVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 105
BCG 1948c EAVNAHP-HADETIFGAVRFALP DVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 105
RHA1_ro05274 EAVHARP-HADETIFGAVRFALP DVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 99
Mvan 2983 EAVEARP-HADDTIFGAVRTALPEVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 100
Franean1DRAFT 1681 TAVYARP-HADDSIVGSVREELPEVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 123
Noca 0874 GAVHALP-HADDSIIGAVREGLPEVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 106
MSMEG 6383 RSVYARP-HADDTVIRAVREALPEVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 102
Mvan 3209 HAVGRHP-HADDELINATRELVPDVSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 105
nfa29490 SVVHEHP-HSDSDILGRVRESVGA VSRQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 102
SCO5561 EIVTRAGD-HLDAEALTSVRRRVGHVSLQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 107
Fur3 EIVTRDGD-HLGVAEALASVDRVGHVSLQAVYDVVHALTAGLLRRFPAGSPARFELATG---DNHHHLVCRACHRTVD 104
AAur 3058 AAVQHHP-HSPAEGILAAARKELPETAQSVVYVLDLTDQLMRLRFPAGSPARFELATG---DNHHHLVCRACHRTVD 106
Arth 3077 TAVERHP-HSPAESILAAAREELPEMTAQSVVYVLDLTDQLMRLRFPAGSPARFELATG---DNHHHLVCRACHRTVD 106
Lxx02790 SALSDRP-HSADETVLAAPALPAGHSIQNHNVLDLTLRMVRRIEPAHSPALVETRVG---DNHHHLVCRACHRTVD 109
Rxy1 1224 EALKAEGHPHSAEDVYLVKRNPRVALGTVYQALSVLEIEGVSEKHWSEPTTRDNLNLEP---HLDTRCVRGKAVE 100
Mjls 1895 ALRRTGLSMSQAVVIRALADHPQASAAELARLCFVTRQSLQDVSTGLRSAGLIDHAQVFPAR---GRARALTTATGRRR 102
ruler90.....100.....110.....120.....130.....140.....150.....160



SAV4029	ADIG-VAAEFIAKLRETF	---GFD---DMKHFAIFGRCCNCAKLSSTTKS	145
SCO4180	ADLS-VAADFAKLRQF	---GFD---DMKHFAIFGRCCESCSLKGSTTS	145
Franean1DRAFT_3571	ISPE-RLAGIVGELRAEL	---GFTVDMDHLLTAGRCACCTAAGRR	144
Acel_0061	VGSE-VVQSLIQRLDDEH	---GFAADVHFHFAIFGRCTCRSTT	150
Noca_4251	VDPE-VIGPLAERLVRDH	---GFVIDVGHIAVFGRCCTDCEEDR	139
Rxyl_1228	FNEE-LMEYLLQVERET	---GFVSDSYEITLHGLCRECAAAG	138
Rxyl_1140	FEEC-PLDGAGLG	---RIG---GFSFRANSLLEVYGRCAAGR	152
AAur_2630	VEAP-AVEIWAARIAAEH	---GFTEVAHTVEIFGLCPECTAKKAAGKL	168
Arth_2638	VEAP-AVEIWAARIAAEH	---GYTEVAHTVEIFGLCPDCTARKADAG	154
MAV_2036	VGDH-EVEEWATAVAAKH	---GFSVDSHTIEIFGTCSECR	135
MAP2139	VGDH-EVEEWATAVAAKH	---GFSVDSHTIEIFGTCSECR	135
Mb2380	VGDH-EVEAWAAEVATKH	---GFSVDSHTIEIFGTCSDCRS	130
BCG_2373	VGDH-EVEAWAAEVATKH	---GFSVDSHTIEIFGTCSDCRS	130
MT2428	VGDH-EVEAWAAEVATKH	---GFSVDSHTIEIFGTCSDCRS	130
Rv2359	VGDH-EVEAWAAEVATKH	---GFSVDSHTIEIFGTCSDCRS	130
MUL_3612	VADH-EVEIWAANVAARH	---GFSVDSHTIEIFGTCSDCRRPGAAALR	137
ML0824	VGDH-EVEAWAAEVAAKH	---GFSVDSHTIEIFGTCSECRS	131
MSMEG_4487	VSGG-DVEIWAQAQVARDH	---GFSVDSHTIEIFGVCQDVERPAGNQT	136
Mvan_3820	IQGG-QVEIWAAEVAHEH	---GFSVDSHTIEIFGLCSNCA---AGN	131
Mjls_3458	IQGG-QVEIWAADIAREH	---GFSVDSHTIEIFGLCGDCSAR	131
Mkms_3510	IQGG-QVEIWAADIAREH	---GFSVDSHTIEIFGLCGDCSAR	131
Mmcs_3447	IQGG-QVEIWAADIAREH	---GFSVDSHTIEIFGLCGDCSAR	131
nfa14570	VAGP-TVEAWADALAGEH	---GFTDVSHTIEIFGTCRDCAERRS	141
RHA1_ro01222	VEGP-TVEQWSQSIADAH	---GFSVDSHTIEIFGLCKDCSATQ	141
SAV5631	VEGP-AVEKWAEEIAAEH	---GYVNVVAHTVEIFGTCACCAAAKS	138
SCO2508	VEGP-AVEKWAEEIAAEH	---GYVNVVAHTVEIFGTCADCAAGSGG	139
Noca_1934	VEGP-AVERWIRAIAAEH	---GYAEVSHTEIFGTCACGG	135
FRAL0074	IAGP-EIEAWIAAIADAE	---GFVDVHTVEIYGTCCAGCAAGAAS	131
Franci3_0061	IAGP-EIEAWIAKVANAE	---GFVDVHTVEIYGTCTICAARPAT	142
Franean1DRAFT_4289	IAGP-EIEAWIASSVASAE	---GFTDVTHTVEIYGTCCARCAASRNSDNSPGRPRGGG	192
Tfu_0856	IEGP-AVESWADELAAQH	---GFVDLTHTEIFGLCSDCAAAPRT	129
Acel_2085	VKGI-SVERWAERVAARA	---GFVDVHTVEIYGTCCPGCAAGR	138
BAD_0517	IES---PSESWLKGISDKY	---GFTIERHTLEVFGLCEDCRKADK	132
BL1128	IDP---PSEAWLRKVADGH	---GFTVESHTLEVFGLCSDCQKEKQAKQAKAVSE	146
Lxxx25010	IEAD-EVEAWARSAAADH	---GFSQVQHVVDVFGLCAGCS---AKADLAASSAVP	138
CE2180	IDGG-PVERWAGEVARTH	---GFSVSSHAEIIFGLCPACRPPDVTVDQQA	175
NCgl2200	IDGG-PVEIWAQEIATKN	---GFALSSHEAEIIFGLCADCKEKVT	144
DIP1710	IDGG-PVEKWAKEVAQLH	---GFQVTGHDAEIVGLCESCSAAE	142
jk0612	IDGG-FVEDWAAEIAKFF	---GYQKSGHTAEIIFGLCGDCKKKSAS	143
PFA0948	IGPEKILEDWIRDLAAY	---EFSETGHELELFGICSECSAVHTRSVS	137
FRAL5117	IDHP-VPDGMAEAIARRS	---GFAITGYDLQFRGMCPCDQANGSDPARAAGGTGPTVNTHAKGALHAEA	146
Franci3_3112	IDHP-VLDGMAAIACRS	---GFAITGYDLRFRGLCPDQANGSGPARGAAGTQQQ	146
Franean1DRAFT_4643	IDHP-VPDGMVAEAIARRS	---GFTITGYDLQFRGLCPECQTAGEGHRPGR	141
FRAL2798	VPAD-LLDGVDRLARQI	---GFRLOQPDHAALVGLCRPAAAADPPD---HPR	177
Franci3_2661	VPAD-LLDDVARRLATTV	---GFTLQPDHAALVGLCRACRCSVTSFSDGDLAPA	173
Rxyl_1144	LPGA-LLRVPAQTLLPG	---GHRVEECSLLLSGSCGCELSREGTR---GPGG	137
SAV3053	VHPS-GNPLADLPDSERF	---GFTVSDVEVTYRGVCPNCAAA	138
SCO5206	VHPH-GNPLADLPDSERF	---GFTVSDVEVTYRGVCPNCAAA	138
Acel_2095	VDCAVGVVPCISPADAAQ	---YLVDEAEVTVWGLCPQCNHRRPSADHGGTITAGPTEKHHVPARGEGGDR	166
Noca_0839	VACATGEAPCLQASDDAG	---YLLDEAEVTVWGLCANQO---AAGELELL	143
Mkms_4974	VDCIVGAAPCLDHAILEDG	---FTVDEAEVVFVWGLCADCRA---EPPAAGASCRIL	108
Mmcs_4885	VDCIVGAAPCLDHAILEDG	---FTVDEAEVVFVWGLCADCRA---EPPAAGASCRIL	108
Mjls_5253	VDCIVGAAPCLLGHPSPRGR	---FHRRRGRSRLGHMGRLSR---G---AAGGRVILPSVTGLA	158
MSMEG_6253	VDCAVGEAPCLPESDLAG	---FAIDAEVTVWGLCADCQH---DS-ATTRPQSSITI	154
FRAL3168	VDCVTEGARPCLEPSDDAG	---FVIEAEVTVWGLVCRDCEP---GDSGSDVPEAR	148
nfa3250	VDCAVGAAPCLPESSETHG	---YAVDEAEVTVWGLCPDCR---AAQD	143
RHA1_ro04308	VDCAVGEAPCLDPSAHHG	---FEIDEAEVTVWGLCSQCRT---GAQSGTGSAAALS	152
Tfu_0145	IDCVVGEAPCLAPSQAHG	---YTVDEAEVTVWGLVCPSCKA---KESEH	140
Mjls_2712	VDCAVGEAPCLMPS-EHDALDGFVLDDEAEVTVWGLCPDCAA	---ESSTADSSRSHP	157
Mmcs_2681	VDCAVGEAPCLMPS-EHDALDGFVLDDEAEVTVWGLCPDCAA	---ESSTADSSRSHP	195
Mkms_2726	VDCAVGEAPCLMPS-EHDALDGFVLDDEAEVTVWGLCPDCAA	---ESSTADSSRSHP	157
MSMEG_3460	VDCAVGEAPCLTFSNDDHALDGFLLDEAEVTVWGLCRECSV	---DGP	146
MAV_2752	VDCAVGEAPCLTFSDDNVLDGFVLDDEAEVTVWGLCADCST	---AGS	134
MAP1669c	VDCAVGEAPCLTFSDDNVLDGFVLDDEAEVTVWGLCAECST	---AGS	146
MUL_2189	IDCAVGEAPCLAPSDDSNVLDGFVLDDEAEVTVWGLMPCDCST	---AMPRSQP	138
Mb1944c	VDCAVGEAPCLTASDHNG	---FLLDEAEVTVWGLCPDCSI---SDTS---RSHP	150
MT1960	VDCAVGEAPCLTASDHNG	---FLLDEAEVTVWGLCPDCSI---SDTS---RSHP	150
Rv1909c	VDCAVGEAPCLTASDHNG	---FLLDEAEVTVWGLCPDCSI---SDTS---RSHP	150
BCG_1948c	VDCAVGEAPCLTASDHNG	---FLLDEAEVTVWGLCPDCSI---SDTS---RSHP	150
RHA1_ro05274	VDCAVGEAPCLTASDDNG	---FLVEAEVTVWGLCPDCST---SQTS---RSNP	144
Mvan_2983	VDCAVGEAPCLVPSDDGSLDGFVLDDEAEVTVWGLCPGCLA	---AEIS---RSHQ	149
Franean1DRAFT_1681	VDCAVGSAPCLAASDDRG	---FSIDEAEVTVWGLCPDCSPPA---TFDRPRAAPDRS	174
Noca_0874	VDCAVGAPCLTASDDHG	---FRIDEAEVTVWGLCPACS---TFRS	146
MSMEG_6383	VDCAVGEAPCLTGSDDHG	---YALDEAEVTVWGLCPACAQ---DPRAKARTSRSHP	153
Mvan_3209	VDCAVGEAPCLTASDDLQ	---FEVDEAEVTVWGLCPACST---APSPQ	147
nfa29490	VDCAVGEAPCLDASHDHG	---FVVDEAEVTVWGLCPDCSK---ALSAPPK	146
SCO0561	VDCAVGDAPCLTASDDRG	---FVIDEAEVTVWGLCPDCST---FGSSPAP	151
FurS	VDCAVGDAPCLTASDDHG	---FAIDEAEVTVWGLCPDCST---GRSS	145
AAur_3058	VDCAVGHAPCLTFHWDSNSKP	---MTIQIADVVMVQGIQDCQS---KQLPVTSHVQK	158
Arth_3077	VDCAVGHAPCLTFHWDSNSKP	---MTIQIADVVMVQGIQDCQR---TQKLPARN	155
Lxxx02790	VDCVGHAPCLR---LSEAAG	---FAVDTAEVTVWGLCPSCQE---STAATPSRE	147
Rxyl_1224	VPGVDAGDLESRIQENTP	---YRVTRATMLLEGVCPAQDG	147
Mjls_1895	LAAAHSAVIAVEEQMLTG	---LSGAECRRLSGLLAAACANLEGE	143

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